

Package ‘MAQCsubset’

April 13, 2017

Title Experimental Data Package: MAQCsubset

Version 1.12.0

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Description Data Package automatically created on Sun Nov 19 15:59:29 2006.

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Depends R (>= 2.10.0), affy (>= 1.23.4), Biobase (>= 2.5.5), lumi,
methods

Suggests genefilter, codelink

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biocViews ExperimentData, MicroarrayData, GEO

LazyLoad true

NeedsCompilation no

R topics documented:

gehMAQCsubDef	1
gnfCerebHi	2
MAQCsubset	3
proboscis	3
proboStruct-class	4
Index	6

gehMAQCsubDef *Excerpt from GE Codelink array contributions to MAQC*

Description

Excerpt from GE Codelink contributions to MAQC

Usage

```
data(gehSubRaw)
data(gehMAQCsubDef)
```

Details

gehSubRaw is a `codeLink::CodeLink` instance based on reading the raw GEO files: "GSM123122_GEH_1_A1.TXT" "GSM123123_GEH_1_A2.TXT" "GSM123127_GEH_1_B1.TXT" "GSM123128_GEH_1_B2.TXT" "GSM123132_GEH_1_C1.TXT" "GSM123133_GEH_1_C2.TXT" "GSM123137_GEH_1_D1.TXT" "GSM123138_GEH_1_D2.TXT"

gehMAQCsubDef is an `ExpressionSet` instance based on default background correction and normalization of the `codeLink` package. The original feature names include duplicates; these were made unique by `make.names` with `unique=TRUE`.

Author(s)

Vince Carey <stvjc@channing.harvard.edu>

Examples

```
data(gehMAQCsubDef)
gehMAQCsubDef
```

gnfCerebHi

Gene lists for hi or low abundance in cerebellum according to Novartis GNF symatlas

Description

Data frames with gene lists for hi or low abundance in cerebellum according to Novartis GNF symatlas

Usage

```
data(gnfCerebHi)
data(gnfCerebLow)
```

Details

The `symatlas.gnf.org` database was searched using the `gcrma` version of human gene atlas for genes having expression in cerebellum at least 3 times (or at most 1/3 times) median expression over all organs surveyed. The resulting gene lists were intersected with genes present on GE `codeLink` (version used in `MAQCsubset`) and `hgu95a`.

Value

`data.frame` instances with columns providing gene name, affy probe set identifier, `codeLink` probe identifier, `illuminaHumanv1` identifier.

Author(s)

Vince Carey <stvjc@channing.harvard.edu>

Examples

```
data(gnfCerebHi)
gnfCerebHi[1:3,]
```

MAQCsubset

Experimental Data Package: MAQCsubset

Description

selected data from the MAQC project (Nature Biotechnology, Sept. 2006)

Usage

```
data(afxsubRMAES)
data(afxsubRMA)
data(afxsub)
```

Format

The format is: An ExpressionSetObject with covariates:

- site: from cel
- samp: rna src/mixture code
- repl: replicate

Note

afxsubRMA is an exprSet (deprecated) and afxsub is an AffyBatch. afxsubRMAES is a proper ExpressionSet instance.

ilmMAQCsubR is the result of applying lumiR to the files in the vicinity of GEO GSM122901 with filename suffixes matching those of the sampleNames in the set.

Examples

```
data(afxsubRMAES)
```

proboscis

Produce a plot similar to Figure 2 of the Shippy MAQC paper (PMID 16964226).

Description

Produce a plot similar to Figure 2 of the Shippy MAQC paper (PMID 16964226).

Usage

```
proboscis(es, site=1, ABp=0.001, CDp=0.01, mmrad=100)
```

Arguments

es	ExpressionSet instance with MAQC assay results
site	numeric code – site to be assessed
ABp	ABp – p-value threshold to declare concentration of gene in sample A to be different from the concentration in sample B
CDp	CDp – p-value threshold to declare concentration of gene in sample C to be different from the concentration in sample D
mmrad	numeric radius of the moving mean used to smooth the proportions differentially expressed

Details

Figure 2 of the Shippy paper consists of a collection of plots of estimated probabilities of self-consistent monotone titration – briefly, samples are such that A has 100% USRNA, B has 100% Ambion brain, C has 75% USRNA+25% brain, D has 25% USRNA, 75% brain. Self-consistent monotone titration holds for gene *g* if microarray measures for that gene satisfy $A > C > D > B$ or $B > C > D > A$. The estimated probability functions look like a creature sticking its nose over a wall, thus the name of this function.

Value

an instance of [proboStruct](#), for which a plot and lines method are available.

Author(s)

Vince Carey <stvjc@channing.harvard.edu>

References

PMID 16964226

Examples

```
data(afxsubRMAES)
NN2 = proboscis(afxsubRMAES, site=2)
plot(NN2)
```

proboStruct-class *Class "proboStruct"*

Description

structure for managing proboscis plot data

Objects from the Class

Objects can be created by calls of the form `new("proboStruct", ...)`.

Slots

.Data: Object of class "list" ~~
call: Object of class "call" ~~

Extends

Class "[list](#)", from data part. Class "[vector](#)", by class "list", distance 2. Class [AssayData-class](#), by class "list", distance 2.

Methods

plot

Note

The proboscis plot shows how the probability of self-consistent monotone titration (SCMT) varies with the spiked difference in concentrations of two mRNA preparations in an MAQC dataset.

Author(s)

V Carey <stvjc@channing.harvard.edu>

References

For Figure 2 of Shippy et al., Using RNA sample titrations... (Nat Biotech, 24(9):1123-1131, Sep 2006)

Examples

```
data(afxsubRMAES)
NN1 = proboscis(afxsubRMAES)
plot(NN1)
showClass("proboStruct")
```

Index

*Topic **classes**

proboStruct-class, 4

*Topic **datasets**

MAQCsubset, 3

*Topic **models**

gehMAQCsubDef, 1

gnfCerebHi, 2

proboscis, 3

afxsub (MAQCsubset), 3

afxsubRMA (MAQCsubset), 3

afxsubRMAES (MAQCsubset), 3

ExpressionSet, 4

gehMAQCsubDef, 1

gehSubRaw (gehMAQCsubDef), 1

gnfCerebHi, 2

gnfCerebLow (gnfCerebHi), 2

ilmMAQCsubR (MAQCsubset), 3

lines, proboStruct-method
(proboStruct-class), 4

list, 5

make.names, 2

MAQCsubset, 3

plot, proboStruct, ANY-method
(proboStruct-class), 4

plot, proboStruct-method
(proboStruct-class), 4

proboscis, 3

proboStruct, 4

proboStruct-class, 4

show, proboStruct-method
(proboStruct-class), 4

vector, 5